



SEQUENCE LISTING

<110> MA, Jing
GUO, Yajun

<120> PREPARATION AND APPLICATION OF
ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS

<130> 549062000200

<140> US 10/723,003
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<160> 68

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 546
<212> DNA
<213> Homo sapiens

<400> 1
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ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg 180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggccgctggc cctggcacag 240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc 300
gtgaacacgg agatacacatt tgtcaccaaa tgtgccttc agccccccccc cagctgtctt 360
cgcttcgtcc agaccaacat ctccccgcctc ctgcaggaga cctccgagca gctggtgccg 420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
gactcctcaa ccctgccacc cccatggagt ccccgcccc tggaggccac agccccgaca 540
gccccg 546

<210> 2
<211> 182
<212> PRT
<213> Homo sapiens

<400> 2
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu
1 5 10 15
Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
20 25 30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
35 40 45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
50 55 60

Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 65 70 75 80
 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
 85 90 95
 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
 100 105 110
 Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
 115 120 125
 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
 130 135 140
 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
 145 150 155 160
 Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
 165 170 175
 Thr Ala Pro Thr Ala Pro
 180

<210> 3
 <211> 1242
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 3
 atgacagtgc tggcgccagc ctggagccca acaacctatc tcctcctgct gctgctgctg 60
 agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac 120
 ttcgtgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg 180
 gcctccaacc tgcaaggacga ggagctctgc gggggctct ggcggctggt cctggcacag 240
 cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc 300
 gtgaacacgg agatacacatt tgtcaccaaa tgtgccttc agccccccccc cagctgtctt 360
 cgcttcgtcc agaccaacat ctccccgctc ctgcaggaga cctccgagca gctggtggcg 420
 ctgaagccct ggatcaactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
 gactcctcaa ccctgccacc cccatggagt ccccgcccc tggaggccac agccccgaca 540
 gccccggagc ccaaattttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 600
 ctcctggggg gaccgtcagt cttcctcttc ccccccaaaac ccaaggacac cctcatgatc 660
 tccccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggte 720
 aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 780
 gagcagtaca acagcacgt a cccgggtggtc tgcgtcctca ccgtcctgca ccaggactgg 840
 ctgaatggca aggagtacaa gtgcaaggc tccaacaaag ccctcccagc ccccatcgag 900
 aaaaccatct ccaaaggccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 960
 tccccggatg agctgaccaa gaaccaggc agcctgaccc gcctggtcaa aggcttctat 1020
 cccagcgaca tcggcgtgga gtggggagac aatgggcagc cggagaacaaa ctacaagacc 1080
 acgcctcccg tgctggactc cgacggctcc ttcttctt acagcaagct caccgtggac 1140
 aagagcaggt ggcagcaggg gaacgtcttc tcatgtccg tgatgtatga ggctctgcac 1200
 aaccactaca cgcagaagag cctctccctg tctcccgta aa 1242

<210> 4
 <211> 414
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 4

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
1 5 10 15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
20 25 30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
35 40 45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
50 55 60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65 70 75 80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
85 90 95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
100 105 110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
115 120 125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
130 135 140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145 150 155 160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
165 170 175
Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
180 185 190
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
195 200 205
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
210 215 220
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
225 230 235 240
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
245 250 255
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
260 265 270
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
275 280 285
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
290 295 300
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
305 310 315 320
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
325 330 335
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
340 345 350
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
355 360 365
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
370 375 380
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
385 390 395 400
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
405 410

<210> 5

<211> 45

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 5
 ggccgtggag gctctggtgg aggcgttca ggaggcggtg gatct 45

<210> 6
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 6
 Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
 1 5 10 15

<210> 7
 <211> 426
 <212> DNA
 <213> Mus musculus

<400> 7
 atcgccgcca ccatggaatg gagttggata tttctttc tcctgtcagg aactgcaggt 60
 gtccactctg aggtccagct gcacgcgtct ggacctgagc tggtaaagcc tggggcttca 120
 gtgaagatgt cctgcaaggc ttctggatac acattacta gctatgttat gcactgggtg 180
 aacgcagaagc ctgggcaggg ctttgactgg attggatata ttgttcctta caatgatggc 240
 actaagtaca atgagaagtt caaaggcaag gccacactga cttcagacaaa atcctccagc 300
 acagcctaca tggagcttag cagactgacc tctgaggact ctgcggctca ttattgtgtc 360
 tacggtagta ggtacgactg gtattnatgt gtctggggcg cagggaccac ggtcaccgtc 420
 tcctca 426

<210> 8
 <211> 138
 <212> PRT
 <213> Mus musculus

<400> 8
 Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
 1 5 10 15
 Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
 20 25 30
 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
 50 55 60
 Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
 65 70 75 80
 Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser
 85 90 95
 Thr Ala Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110

Tyr Tyr Cys Val Tyr Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp
115 120 125
Gly Ala Gly Thr Thr Val Thr Val Ser Ser
130 135

<210> 9
<211> 465
<212> DNA
<213> Mus musculus

<400> 9
atcatcacca gaacagctta cgagcagacc gccagacagc tcacagggat caagcttgcc 60
gccaccatgg aatcacagac tcaggtcttc ctctccctgc tgctctgggt atctggtacc 120
tgtggaca ttatgtgac acagtgcaca tcatctctgg ctgtgtctgc aggagaaaag 180
gtcaactatga gctgtaagtc cagtcaaagt gttttataca gttcaaatca gaagaactac 240
ttggcctgg accagcagaa accagggcag tctcctaaac tgctgatcta ctgggcatcc 300
actaggaaat ctggtgtccc tgatcgcttc acaggcagtg gatctggac agattttact 360
cttaccatca gcagtgtaca agctgaagac ctggcagttt attactgtca tcaatatttc 420
tcctcataca cgttcgagg ggggaccaag ctggaaataa agcgg 465

<210> 10
<211> 133
<212> PRT
<213> Mus musculus

<400> 10
Met Glu Ser Gln Thr Gln Val Phe Leu Ser Leu Leu Leu Trp Val Ser
1 5 10 15
Gly Thr Cys Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala
20 25 30
Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
35 40 45
Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
50 55 60
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80
Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
85 90 95
Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
100 105 110
Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys
115 120 125
Leu Glu Ile Lys Arg
130

<210> 11
<211> 2021
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 11
atcgccgcca ccatggaatg gagttggata tttctcttc tcctgtcagg aactgcaggt 60

gtccactctg aggtccagct gcagcagtct ggacctgagc tggtaaagcc tggggcttca 120
 gtgaagatgt cctgcaaggc ttctggatac acattcacta gctatgttat gcactgggtg 180
 aagcagaagc ctgggcaggg ccttgactgg attggatata ttgttcctta caatgatggc 240
 actaagtaca atgagaagtt caaaggcaag gccacactga cttcagaccaa atcctccagc 300
 acagcctaca tggagctcag cagactgacc tctgaggact ctgcggctca ttattgtgtc 360
 tacggtagta ggtacgactg gtattnagat gtctggggcg cagggaccac ggtcaccgtc 420
 tcctcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
 tctggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
 gtgtcttggc actcaggcgc cctgaccaggc ggcgtgcaca cttcccggc tgcctacag 600
 tcctcaggac tctactccct cagcagcgtg gtgaccgtc cttccagcag cttgggcacc 660
 cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720
 ggtgagaggc cagcacaggg agggaggggtg tctgctggaa gcaggctcag cgctcctgcc 780
 tggacgcata ccggctatgc agccccagtc cagggcagca aggccaggccc cgtctgcctc 840
 ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggcttttc 900
 ccaggctctg ggcaggcaca ggcttaggtgc ccctaaccca ggccctgcac acaaagggc 960
 aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgcctc ctgacctaag 1020
 cccacccaa aggccaaact ctccactccc tcagctcgga cacctctct cctccagat 1080
 tccagtaact cccaatcttc tctctgcaga gcccaaactt tgtgacaaaaa ctcacacatg 1140
 cccaccgtgc ccaggttaagc cagcccaggc ctcgcctcc agctcaaggc gggacaggtg 1200
 cccttagagta gcctgcatacc agggacaggc cccagccggg tgctgacacg tccacctcca 1260
 tcttcctc agcacctgaa ctccctgggg gaccgtcagt cttcctcttc ccccaaaaac 1320
 ccaaggacac cctcatgatc tcccgaccc ctgagggtcac atgcgtggg gtggacgtga 1380
 gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
 ccaagacaaa gccgcgggag gagcagtaca acagcacgta cccgggtggc tgctcctca 1500
 ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggc tccaacaaag 1560
 ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtgggggtc 1620
 gagggccaca tggacagaggc cccggctcgcc ccaccctctg ccctgagagt gaccgctgta 1680
 ccaacctctg tcctacaggc cagccccgag aaccacaggt gtacaccctg ccccatccc 1740
 gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca 1800
 ggcacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc 1860
 ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga 1920
 gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc 1980
 actacacgca gaagagcctc tccctgtctc ccggtaaatg a 2021

<210> 12
 <211> 468
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 12
 Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
 1 5 10 15
 Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
 20 25 30
 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
 50 55 60
 Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
 65 70 75 80
 Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser
 85 90 95
 Thr Ala Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110

Tyr Tyr Cys Val Tyr Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp
 115 120 125
 Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 130 135 140
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 145 150 155 160
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 165 170 175
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 180 185 190
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 195 200 205
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 210 215 220
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
 225 230 235 240
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 245 250 255
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 260 265 270
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 275 280 285
 His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu
 290 295 300
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 305 310 315 320
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 325 330 335
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 340 345 350
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 355 360 365
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 370 375 380
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 385 390 395 400
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 405 410 415
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 420 425 430
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 435 440 445
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 450 455 460
 Ser Pro Gly Lys
 465

<210> 13
 <211> 786
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 13

atcatcacca gaacagctta cgagcagacc gccagacagc tcacagggat caagctgcc 60
gccaccatgg aatcacagac tcaggtcttc ctctccctgc tgctctgggt atctgttacc 120
tgtggaaaca ttatgtatgc acagtcgcca tcatctctgg ctgtgtctgc aggagaaaaag 180
gtcaactatga gctgtaaatgc cagtcaaagt gtttataaca gttcaaatca gaagaactac 240
ttggcctgggt accagcagaa accaggcag ttcctaaac tgctgatcta ctggccatcc 300
actagggat ctgggtgtccc tgatcgcttc acaggcagtg gatctgggac agattttact 360
cttaccatca gcagtgtaca agctgaagac ctggcagttt attactgtca tcaatatttc 420
tcctcataca cggtcgagg ggggaccaag ctggaaataa agcggactgt ggctgcacca 480
tctgtcttca tcttcccgcc atctgatgag cagttgaaat ctggactgc ctctgttg 540
tgcctgctga ataacttcta tcccaagagag gccaaagtac agtggaaaggt ggataacgcc 600
ctccaatcggt gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac 660
agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaaacacaa agtctacgcc 720
tgcgaagtca cccatcaggg cctgagctcg cccgtcacaa agagcttcaa caggggagag 780
tgtag 786

<210> 14
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 14
Met Glu Ser Gln Thr Gln Val Phe Leu Ser Leu Leu Trp Val Ser
1 5 10 15
Gly Thr Cys Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala
20 25 30
Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
35 40 45
Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
50 55 60
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80
Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
85 90 95
Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
100 105 110
Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gly Thr Lys
115 120 125
Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
130 135 140
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145 150 155 160
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
165 170 175
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
180 185 190
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
195 200 205
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
210 215 220
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 15

<211> 426
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 15
 agagccgcca ccatggattg ggtgtggacc ttgctattcc tggcgtcagt aactgcaggt 60
 gtccactccc aggtgcagct ggtgcagtct ggccgtggag tggccagcc cggccgcagc 120
 ctgaggctgt cctgcaaggc atctggctac accttcacca gctacgtat gacatgggtg 180
 cgccaaagccc ccggaaaaggc cctcgaatgg attggctaca ttgtgcctta taatgacgg 240
 actaagtaca atgaaaagtt caagggcaga tttacaatat caagtgacaa gagcaagtca 300
 accgcattcc tccaaatggc cagttgcgt ccagaggaca ccgccgtata ctattgtgtg 360
 cgcggcagcc gttacgactg gtacttggac tactggggcc aaggcactcc agtcaccgtc 420
 tcctct 426

<210> 16
 <211> 138
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 16
 Met Asp Trp Val Trp Thr Leu Leu Phe Leu Leu Ser Val Thr Ala Gly
 1 5 10 15
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln
 20 25 30
 Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60
 Glu Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
 65 70 75 80
 Glu Lys Phe Lys Gly Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser
 85 90 95
 Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp
 115 120 125
 Gly Gln Gly Thr Pro Val Thr Val Ser Ser
 130 135

<210> 17
 <211> 465
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 17
 gaggattacc ggccatactc atcaccatcc caggatatct ctagaaagct tgccgccacc 60
 atggattttc aagtgcagat tttcagtttc ctgctaatca gtgcgttcactataatgtcc 120

agaggaaaca tcatgatgac tcagagccca tccagcttga gcgcatcagt aggcgaccgc 180
gtaacgatca cttgcaaata ctctcagtca gtattgtact ccagcaacca gaagaactac 240
ctggccggat atcagcagac tcccggcaaa gccccaaagt tgctgattta ttggcctcc 300
acgcgcgagt ctggcgtgcc atcacgctt agcggcagcg ggtccggtaa agattacacg 360
tttaccatta gcagtctgca gcctgaggac atagccaccc actactgtca ccagacttt 420
agttcctaca ctttggcca ggaaactaaa ctgcagatta ctgcga 465

<210> 18
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 18
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser
20 25 30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser
35 40 45
Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
50 55 60
Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser
65 70 75 80
Thr Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
85 90 95
Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
100 105 110
Thr Tyr Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gln Gly
115 120 125
Thr Lys Leu Gln Ile Thr Arg
130 135

<210> 19
<211> 2021
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 19
agagccgcca ccatggattg ggtgtggacc ttgctattcc tggcttcagt aactgcagg 60
gtccactccc aggtgcagct ggtgcagtct ggcgggtggag tggccagcc cggccgcagc 120
ctgaggctgt cctgcaaggc atctggctac accttcacca gctacgtat gacatgggtg 180
cgccaagccc cccgaaaggc cctcgaatgg attggctaca ttgtgcctt taatgacgg 240
actaagtaca atgaaaagtt caagggcaga tttacaatat caagtgcacaa gagcaagtca 300
accgcattcc tccaaatggc cagcttgcgt ccagaggaca cccgcgtata ctattgttg 360
cgccgcagcc gttacgcactg gtacttggac tactggggcc aaggcactcc agtcaccgtc 420
tcctctgtca gcaccaaggc cccatcggtc ttccccctgg caccctccctc caagagcacc 480
tctggggca cagcggccct gggctgcctg gtcaaggact acttccccca accggtgacg 540
gtgtcttggc actcaggcgc cctgaccaggc ggcgtgcaca cttccggc tgcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cttccagcag cttggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720

ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggcttag cgctcctgcc 780
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 ttcacccgga gcctctgcc gccccactca tgctcaggga gagggtcttc tggcttttc 900
 ccaggtctg ggcaggcaca ggctaggtgc ccctaaccac ggcctgcac acaaaggggc 960
 aggtgctggg ctcagaccc ccaagagcca tatccggag gaccctgccc ctgacctaag 1020
 cccaccccaa aggccaaact ctccactccc tcagctcga caccttctc cctccagat 1080
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 ggcacatgc cgtggagtg gagagcaatg ggcagccga gaacaactac aagaccacgc 1860
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 gcaggtggca gcaggggaac gtcttctcat gtcctgtat gcatgaggct ctgcacaacc 1980
 actacacgca gaagagcctc tccctgtctc ccggtaatg a 2021

<210> 20
 <211> 468
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 20
 Met Asp Trp Val Trp Thr Leu Leu Phe Leu Leu Ser Val Thr Ala Gly
 1 5 10 15
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln
 20 25 30
 Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60
 Glu Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
 65 70 75 80
 Glu Lys Phe Lys Gly Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser
 85 90 95
 Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp
 115 120 125
 Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 130 135 140
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 145 150 155 160
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 165 170 175
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 180 185 190
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr

195	200	205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn		
210	215	220
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser		
225	230	235
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu		
245	250	255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu		
260	265	270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser		
275	280	285
His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu		
290	295	300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr		
305	310	315
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn		
325	330	335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro		
340	345	350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln		
355	360	365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val		
370	375	380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val		
385	390	395
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro		
405	410	415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr		
420	425	430
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val		
435	440	445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu		
450	455	460
Ser Pro Gly Lys		
465		

<210> 21
 <211> 786
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 21
 gagcattacc ggccatactc atcaccatcc caggatatct ctagaaagct tgccgccacc 60
 atggattttc aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcc 120
 agaggaaaca tcatgtatgac tcagagccca tccagcttga ggcgcattcgtt aggcgaccgc 180
 gtaacgatca cttgcaaatc ctctcagtca gtattgtact ccagcaaccca gaagaactac 240
 ctggccggat atcagcagac tcccggcaaa gccccaaagt tgctgattta ttgggcctcc 300
 acgcgcgagt ctggcgatcc atcacgctt agcggcagcg ggtccggatc agattacacg 360
 tttaccatta gcagtctgca gcctgaggac atagccacct actactgtca ccagacttt 420
 agttcctaca cttttggcca gggaaactaaa ctgcagatca ctcgaactgtt ggctgcacca 480
 tctgtcttca tcttcccgcc atctgatgag cagttaaat ctggaaactgc ctctgttg 540
 tgccctgatca ataacttcta tcccagagag gccaaagtac agtggaaagg ggataacgcc 600
 ctccaatcggtt gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac 660

agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc 720
tgcaagtca cccatcaggg cctgagctcg cccgtcacaa agagcttcaa caggggagag 780
tgttag 786

<210> 22
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 22
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser
20 25 30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser
35 40 45
Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
50 55 60
Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser
65 70 75 80
Thr Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
85 90 95
Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
100 105 110
Thr Tyr Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gln Gly
115 120 125
Thr Lys Leu Gln Ile Thr Arg Thr Val Ala Ala Pro Ser Val Phe Ile
130 135 140
Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
145 150 155 160
Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
165 170 175
Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
180 185 190
Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
195 200 205
Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
210 215 220
His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
225 230 235 240
Cys

<210> 23
<211> 2489
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 23
agagccgcca ccatggattg ggtgtggacc ttgctattcc tgggtcagt aactgcaggt 60

gtccactccc aggtgcagct ggtgcagtct ggccgtggag tggccagcc cggccgcagc 120
 ctgaggctgt cctgcaaggc atctggctac accttcacca gctacgtat gacatgggt 180
 cgccaagccc ccggaaaggg cctcgaaatgg attggctaca ttgtgcctt taatgacggt 240
 actaagtaca atgaaaagtt caagggcaga tttacaatat caagtgacaa gagcaagtca 300
 accgcattcc tccaaatgga cagcttgcgt ccagaggaca cccgcgtata ctattgtgt 360
 cgccgcagcc gttacgactg gtacttggac tactggggcc aaggcactcc agtcaccgtc 420
 tcctctgcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
 tctggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
 gtgtcttggc actcaggcgc cctgaccgc ggcgtgcaca cttcccgcc tgccttacag 600
 tcctcaggac tctactccct cagcagcgtg gtgaccgtc cttccagcag cttgggcacc 660
 cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720
 ggtgagaggg cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc 780
 tggacgcattc cccgctatgc agccccagtc cagggcagca aggccggccc cgtctgcctc 840
 ttcacccgga gcctctgccc gccccactca tgctcaggga gagggttcc tggcttttc 900
 ccaggctctg ggcaggcaca ggcttaggtgc ccctaaccctt ggccctgcac acaaaggggc 960
 aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgcctc ctgacctaag 1020
 cccacccaa aggccaaact ctccactccc tcagctcgga cacctctt cctccagat 1080
 tccagtaact cccaatctt tctctgcaga gcccaaattt tgcacaaaaa ctcacacatg 1140
 cccaccgtgc ccaggtaagc cagcccaggc ctcgcctcc agctcaaggc gggacaggtg 1200
 cccttagagta gcctgcattcc agggacaggc cccagccggg tgctgacacg tccacacttca 1260
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 ccaaggacac cctcatgatc tcccgaccc ctgagggtcac atgcgtggg gtggacgtga 1380
 gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
 ccaagacaaa gccgcgggag gagcagtaca acagcacgtt cccgggtggc tgctcctca 1500
 ccgtccctgca ccaggactgg ctgaatggca aggactacaa gtgcagggtc tccacaaaag 1560
 ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtgggtgc 1620
 gagggccaca tggacagagg cccgctcgcc ccaccctctg ccctgagagt gaccgctgtt 1680
 ccaacctctg tcctacaggc cagccccgag aaccacaggt gtacaccctg ccccatccc 1740
 gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaggc ttctatccca 1800
 ggcacatcgc cgtggagtgg gagagcaatg ggcagccggaa gacaactac aagaccacgc 1860
 ctcccgtctt ggactccgac ggctccttcc tcctctacag caagctcacc gtggacaaga 1920
 gcaggtggca gcaggggaac gtcctctcat gtcgggtat gcatgaggct ctgcacaacc 1980
 actacacgca gaagaggctc tccctgtctc ccggtaaaaac ccaggactgc tccttccaac 2040
 acagccccat tcctccgac ttcgctgtca aaatccgtt gctgtctgac tacctgttcc 2100
 aagattaccc agtcaccgtt gtcctcaacc tgcaggacga ggagctctgc gggggctct 2160
 ggccgcttgtt cctggcacag cgtggatgg agcggctcaa gactgtcgct gggtccaaga 2220
 tgcaaggctt gctggagcgc gtgaacacgg agatacactt tgcacaaaaa tgccttcc 2280
 agccccccccc cagctgttcc cgttcgtcc agaccaacat ctcccgccctc ctgcaggaga 2340
 cctccgagca gctgggtggcg ctgaaggccct ggtactactg ccagaacttc tcccggtgcc 2400
 tggagctgca gtgtcagccc gactcctcaa ccctgcccacc cccatggagt ccccgcccc 2460
 tggaggccac agccccgaca gccccgtga 2489

<210> 24

<211> 624

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 24

Met Asp Trp Val Trp Thr Leu Leu Phe Leu Leu Ser Val Thr Ala Gly

1	5	10	15
---	---	----	----

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln

20	25	30
----	----	----

Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe

35	40	45
----	----	----

Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60
 Glu Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
 65 70 75 80
 Glu Lys Phe Lys Gly Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser
 85 90 95
 Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp
 115 120 125
 Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 130 135 140
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 145 150 155 160
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 165 170 175
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 180 185 190
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 195 200 205
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 210 215 220
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
 225 230 235 240
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 245 250 255
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 260 265 270
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 275 280 285
 His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu
 290 295 300
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 305 310 315 320
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 325 330 335
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 340 345 350
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 355 360 365
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 370 375 380
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 385 390 395 400
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 405 410 415
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 420 425 430
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 435 440 445
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 450 455 460
 Ser Pro Gly Lys Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser
 465 470 475 480
 Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln
 485 490 495
 Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys

500	505	510	
Gly Gly Leu Trp Arg Leu Val	Leu Ala Gln Arg Trp	Met Glu Arg Leu	
515	520	525	
Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu	Glu Arg Val Asn		
530	535	540	
Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser			
545	550	555	560
Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr			
565	570	575	
Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe			
580	585	590	
Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro			
595	600	605	
Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro			
610	615	620	

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<210> 25
<211> 2534
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic Construct

<400> 25
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gtccactccc aggtgcagct ggtgcagtc ggcgggtggag tggccagcc cggccgcagc 120
ctgaggctgt cctgcaaggc atctggctac accttcacca gctacgtat gacatgggtg 180
cgccaagccc ccggaaaggg cctcgaatgg attggctaca ttgtgccta taatgacggt 240
actaagtaca atgaaaagtt caagggcaga tttacaatat caagtgacaa gagcaagtc 300
accgcattcc tccaaatggc cagcttgcgt ccagaggaca cgcgcgtata ctattgtgtg 360
cgcggcagcc gttacgactg gtacttggac tactggggcc aaggactcc agtcaccgtc 420
tcctctgcta gcaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc 480
tctggggca cagcggccct gggctgcctg gtcaaggact actttcccgta accggtgacg 540
gtgtcttggc actcaggcgc cctgaccagc ggctgcaca cttttccggc tgccttacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cttccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720
ggtgagaggc cagcacaggg agggagggtg tctgtggaa gcaggtctag cgctcctgcc 780
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aggtgctggg ctcagacactg ccaagagcca tatccgggag gaccctgccc ctgacctaag 1020
cccaccccaa aggccaaact ctccactccc ttagctcgga caccttctc cctcccaagat 1080
tccagtaact cccaatcttc tctctgcaga gcccaaattt tggacaaaaa ctcacacatg 1140
cccacccgtgc ccaggttaagc cagccccaggc ctgccttc agctcaaggc gggacaggtg 1200
cccttagagta gcctgcattcc agggacaggg cccagccggg tgctgacacg tccacacctca 1260
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ccaagacaaa gcccggggag gagcagtaca acagcacgtc ccgggtggtc tgctccctca 1500
ccgtccctgca ccaggactgg ctgaatggca aggagtacaa gtcaaggtc tccaacaaag 1560
ccctcccccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtgggggtgc 1620
gagggccaca tggacagagg ccggctcggt ccaccctctg ccctgagagt gaccgctgt 1680
ccaacctctg tcctacaggg cagccccag aaccacagggt gtacaccctg ccccccattcc 1740
gggatgagct gaccaagaac caggtcagcc tgacctgct ggtcaaaggc ttctatccca 1800
gcgacatcgc cgtggagtgg gagagaatg ggcagccggc gaacaactac aagaccacgc 1860

ctcccggtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga 1920
gcagggtaac gcagggtggca gtcgttctcat gtcgggtat gcatgaggct ctgcacaacc 1980
actacacgca gaagagcctc tccctgtctc ccggtaaagg cggtgaggc tctgggtggag 2040
gcggttcagg aggcgggtgga tctaccagg actgctcctt ccaacacagc cccatctcct 2100
ccgacttcgc tgtcaaaaatc cgtagctgt ctgactacct gcttcaagat taccaggatca 2160
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cacagcgctg gatggagcgg ctcaagactg tcgctgggtc caagatgcaa ggcttgcgtgg 2280
agcgcgtgaa cacggagata cacttgtca ccaaattgtgc ctttcagccc ccccccagct 2340
gtcttcgctt cgtagcggacc aacatctccc gcctcctgca ggagacctcc gageagctgg 2400
tggcgctgaa gcccctggatc actcgccaga acttctccc gtgcctggag ctgcagtgtc 2460
agcccgactc ctcaaccctg ccaccccat ggagtccccg gcccctggag gccacagccc 2520
cgacagcccc gtga 2534

<210> 26
<211> 639
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 26
Met Asp Trp Val Trp Thr Leu Leu Phe Leu Leu Ser Val Thr Ala Gly
1 5 10 15
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Val Val Gln
20 25 30
Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45
Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60
Glu Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65 70 75 80
Glu Lys Phe Lys Gly Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser
85 90 95
Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val
100 105 110
Tyr Tyr Cys Ala Arg Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp
115 120 125
Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
130 135 140
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145 150 155 160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
165 170 175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
180 185 190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
195 200 205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
210 215 220
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
225 230 235 240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
245 250 255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
260 265 270

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 275 280 285
 His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu
 290 295 300
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 305 310 315 320
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 325 330 335
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 340 345 350
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 355 360 365
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 370 375 380
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 385 390 395 400
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 405 410 415
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 420 425 430
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 435 440 445
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 450 455 460
 Ser Pro Gly Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 465 470 475 480
 Gly Gly Ser Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser
 485 490 495
 Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp
 500 505 510
 Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly
 515 520 525
 Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys
 530 535 540
 Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr
 545 550 555 560
 Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys
 565 570 575
 Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser
 580 585 590
 Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser
 595 600 605
 Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro
 610 615 620
 Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro
 625 630 635

<210> 27
 <211> 1986
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 27

atgacagtgc tggcgccagc ctggagccca acaacctatc tcctcctgct gctgctgctg 60
agctcgggac tcagtggtac ccaggactgc tccttccaac acagccccat ctcctccgac 120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg 180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag 240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc 300
gtgaacacgg agatacactt tgcacccaaa tgcacccccc agccccccc cagctgtctt 360
cgcttcgtcc agaccaacat ctcccgctc ctgcaggaga cctccgagca gctggtggcg 420
ctgaagccct ggatcactcg ccagaacttc tcccgggtgc tggagctgca gtgtcagccc 480
gactcctcaa ccctgccacc cccatggagt ccccgcccc tggaggccac agccccgaca 540
gccccggagc ccaaatttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 600
ctcctggggg gaccgtcagt ctcccttgc ccccaaaaac ccaaggacac cctcatgatc 660
tcccgaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggc 720
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 780
gagcagtaca acagcacgt a cccgggtgc tgcgtcctca cctgcctgca ccaggactgg 840
ctgaatggca aggagtacaa gtcaaggct tccaacaaag ccctcccagc ccccatcgag 900
aaaaccatct ccaaaggccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 960
tcccgatg agctgaccaa gaaccaggc agcctgaccc gcctggtaaa aggcttctat 1020
cccaagcgaca tcgcccgtga gtggagagc aatgggcage cggagaacaa ctacaagacc 1080
acgcctcccg tgctggactc cgacggctcc ttcttctt acagcaagct caccgtggac 1140
aagagcagg ggcagcaggg gaacgtcttc tcatgtccg tgcatgtac ggctctgcac 1200
aaccactaca cgcagaagag cctctccctg tctcccgta aacaggtgca gctggtgag 1260
tctggcggtg gagtggtcca gcccggccgc agcctgaggc tgcgtcctca ggcacatctggc 1320
tacacccatca ccagctacgt gatgacatgg gtgcgtccaa gggccctcgaa 1380
tggattggct acattgtgcc ttataatgac ggtactaagt acaatgaaaa gttcaaggc 1440
agatttacaa tatcaagtga caagagcaag tcaaccgc tccctccaaat ggacagctt 1500
cgtccagagg acaccggcgt atactattgt gtgcgtccaa ggcgttacga ctggacttt 1560
gactactggg gccaaggcac tccagtcacc gtctcctctg ggggtggagg ctctggtgga 1620
ggcggttcag gaggcgggtgg atctaaccatc atgatgactc agagccatc cagcttgagc 1680
gcatcagtag ggcaccgcgt aacgatcact tgcacccatc ctcagtcagt attgtactcc 1740
agcaaccaga agaactaccc ggcggatata cagcagactc cccgcaaaagc cccaaagtt 1800
ctgattttt gggccctccac ggcgtccat cgcgtttag cggcagcggg 1860
tccggtagg attacacgtt taccattagc agtctgcagc ctgaggacat agccacctac 1920
tactgtcacc agtactttt tag ttcctacact tttggccagg gaactaaact gcagattact 1980
cgatga 1986

<210> 28
<211> 661
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 28
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
1 5 10 15
Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
20 25 30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
35 40 45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
50 55 60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65 70 75 80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
85 90 95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala

100	105	110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser		
115	120	125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp		
130	135	140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro		
145	150	155
Asp Ser Ser Thr Leu Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala		
165	170	175
Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr		
180	185	190
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe		
195	200	205
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro		
210	215	220
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val		
225	230	235
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr		
245	250	255
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val		
260	265	270
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys		
275	280	285
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser		
290	295	300
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro		
305	310	315
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val		
325	330	335
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly		
340	345	350
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp		
355	360	365
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp		
370	375	380
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His		
385	390	395
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gln Val		
405	410	415
Gln Leu Val Gln Ser Gly Gly Val Val Gln Pro Gly Arg Ser Leu		
420	425	430
Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Val Met		
435	440	445
His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr		
450	455	460
Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys Gly		
465	470	475
Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser Thr Ala Phe Leu Gln		
485	490	495
Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg		
500	505	510
Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp Gly Gln Gly Thr Pro		
515	520	525
Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly		
530	535	540
Gly Gly Gly Ser Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ser		
545	550	555
		560

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser
 565 570 575
 Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
 580 585 590
 Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 595 600 605
 Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 610 615 620
 Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr
 625 630 635 640
 Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys
 645 650 655
 Leu Gln Ile Thr Arg
 660

<210> 29
 <211> 2489
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 29
 cttgccgcca ccatggaatg gagttggata tttcttttc tcctgtcagg aactgcaggt 60
 gtccactctg aggtccagct gcagcagtct ggacctgagc tggtaaagcc tgggcttca 120
 gtgaagatgt cctgcaaggc ttctggatac acattacta gctatgttat gcactgggtg 180
 aaggagaagc ctgggcaggg ctttgactgg attggatata ttgttcctta caatgatggc 240
 actaagtaca atgagaagtt caaaggcaag gccacactga cttcagaccaa atcctccagc 300
 acagcctaca tggagctcag cagactgacc tctgaggact ctgcggctca ttattgtgtc 360
 tacggtagta ggtacgactg gtattnagat gtctggggcg cagggaccac ggtcaccgtc 420
 tcctcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
 tctggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
 gtgtcttggc actcaggcgc cctgaccaggc ggcgtgcaca cttcccgcc tgcctacag 600
 tcctcaggac tctactccct cagcagcgtg gtgaccgtc cttccagcag cttgggcacc 660
 cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720
 ggtgagggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgccc 780
 tggacgcata ccggctatgc agccccagtc cagggcagca aggccaggccc cgtctgcctc 840
 ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggcttttc 900
 ccaggctctg ggcaggcaca ggcttaggtgc ccctaaccac ggcctgcac acaaaggggc 960
 aggtgctggg ctcagacactg ccaagagcaca tatccgggag gaccctgccc ctgacctaag 1020
 cccacccaa aggccaaact ctccactccc tcagctcgga cacctctt cctccagat 1080
 tccagtaact cccaatctt tctctgcaga gccccaaatct tgtgacaaaaa ctcacacatg 1140
 cccaccgtgc ccaggtaaagc cagcccaggc ctcgcctcc agctcaaggc gggacaggtg 1200
 cccttagagta gcctgcatacc agggacaggc cccagccggg tgctgacacg tccacctcca 1260
 tctttcctc agcacctgaa ctccctgggg gaccgtcagt cttccctt ccccaaaaac 1320
 ccaaggacac cctcatgatc tcccgaccc ctgagggtcac atgcgtgggt gtggacgtga 1380
 gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
 ccaagacaaa gccgcgggag gagcagtaca acagcacgtc cccgggtggc tgcgtcctca 1500
 ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaagggtc tccacacaaag 1560
 ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtgggggtgc 1620
 gagggccaca tggacagagg ccggctcgcc ccaccctctg ccctgagagt gaccgctgtc 1680
 ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg ccccatcccc 1740
 gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatcccc 1800
 ggcacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc 1860
 cttccgtctt gactccgac ggctccttct tcctctacag caagctcacc gtggacaaga 1920

gcaggtggca gcaggggaac gtcttctcat gctccgtat gcatgaggct ctgcacaacc 1980
 actacacgca gaagagcctc tcctgtctc ccggtaaaac ccaggactgc tccttccaac 2040
 acagccccat ctccctccgac ttcgctgtca aaatccgtga gctgtctgac tacctgcttc 2100
 aagattaccc agtcaccgtg gcctccaacc tgcaggacga ggagctctgc gggggcctct 2160
 ggcggctggc cctggcacag cgctggatgg agcggctcaa gactgtcgct gggtccaaga 2220
 tgcaaggctt gctggagcgc gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc 2280
 agcccccccc cagctgtctt cgcttcgtcc agaccaacat ctcccgccctc ctgcaggaga 2340
 cctccgagca gctggggcg ctgaagccct ggatcaactcg ccagaacttc tcccggtgcc 2400
 tggagctgca gtgtcagccc gactcctcaa ccctgccacc cccatggagt ccccgcccc 2460
 tggaggccac agccccgaca gccccgtga 2489

<210> 30
 <211> 624
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 30
 Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Ser Gly Thr Ala Gly
 1 5 10 15
 Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
 20 25 30
 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
 50 55 60
 Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
 65 70 75 80
 Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser
 85 90 95
 Thr Ala Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110
 Tyr Tyr Cys Val Tyr Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp
 115 120 125
 Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 130 135 140
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 145 150 155 160
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 165 170 175
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 180 185 190
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 195 200 205
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 210 215 220
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
 225 230 235 240
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 245 250 255
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 260 265 270
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 275 280 285
 His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu

290	295	300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr		
305	310	315
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn		320
325	330	335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro		
340	345	350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln		
355	360	365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val		
370	375	380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val		
385	390	395
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro		
405	410	415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr		
420	425	430
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val		
435	440	445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu		
450	455	460
Ser Pro Gly Lys Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser		
465	470	475
Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln		
485	490	495
Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys		
500	505	510
Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu		
515	520	525
Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn		
530	535	540
Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser		
545	550	555
Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr		
565	570	575
Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe		
580	585	590
Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro		
595	600	605
Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro		
610	615	620

<210> 31
<211> 2534
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 31
cttgcggcca ccatggaatg gagttggata tttctttc tcctgtcagg aactgcaggt 60
gtccactctg aggtccagct gcagcagtct ggacctgagc tggtaaagcc tggggcttca 120
gtgaagatgt cctgcaaggc ttctggatac acattcacta gctatgttat gcactgggtg 180
aaggagaaggc ctgggcaggg ccttgactgg attggatata ttgttcctta caatgatggc 240
actaagtaca atgagaagtt caaaggcaag gccacactga cttcagacaa atcctccagc 300

acagcctaca tggagcttag cagactgacc tctgaggact ctgcggctca ttatttgtc 360
 tacggtagta ggtacgactg gtattnagat gtctggcg cagggaccac ggtcaccgtc 420
 tcctcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
 tctggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
 gtgtcttggta actcaggcgc cctgaccagc ggcgtgcaca cttcccgcc tgcctacag 600
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cttccagcag cttggcacc 660
 cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720
 ggtgagaggg cagcacaggg agggagggtg tctgctggaa gcaggcttag cgctcctgcc 780
 tggacgcata cccgctatgc agccccagtc cagggcagca aggaggccc cgtctgcctc 840
 ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggcttttc 900
 ccaggctctg ggcaggcaca ggctaggtgc ccctaaccctt ggccctgcac acaaaggccc 960
 aggtgctggg ctcagacactg ccaagagcca tatccggag gaccctgccc ctgacctaag 1020
 cccacccaa aggccaaact ctccactccc tcagctcgga caccttctt cctccagat 1080
 tccagtaact cccaatctt tctctgcaga gcccaaattt tttttttttt tttttttttt 1140
 cccaccgtgc ccaggtaagc cagcccaggc ctcgcctcc agctcaaggc gggacaggtg 1200
 cccttagagta gcctgcattcc agggacaggc cccagccggg tgctgacacg tccacctcca 1260
 tcttttccctc agcacctgaa ctccctgggg gaccgtcagt ctcccttcc cccccaaaac 1320
 ccaaggacac cctcatgatc tcccgaccc ctgaggtaact atgcgtgggt gtggacgtga 1380
 gccacgaaga ccctgaggta aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
 ccaagacaaa gccgcgggag gagcagtaca acagcacgtt cccgggtggc tgcgtcctca 1500
 ccgtcctgca ccaggactgg ctgaatggca aggatcaca gtgcaaggc tccaaacaaag 1560
 ccctcccagc cccatcgag aaaaccatct ccaagccaa aggtgggacc cgtgggggtgc 1620
 gagggccaca tggacagagg cccgctcgcc ccaccctctg ccctgagagt gaccgctgta 1680
 ccaacctctg tcctacaggc cagccccag aaccacagggt gtacaccctg ccccatcccc 1740
 gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca 1800
 ggcacatcgc cgtggagtg gggatgagct gaccaagaac caggtcagcc tgacctgcct 1860
 ctcctgtgt ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga 1920
 gcaggtggca gcaggggaaac gtcttctcat gctccgtat gcatgaggct ctgcacaacc 1980
 actacacgca gaagagcctc tccctgtctc ccggtaaagg cgggtggaggc tctggggag 2040
 gcggttcagg aggcgggtgg tctaccctagg actgctcctt ccaacacagc cccatctcct 2100
 ccgacttcgc tgcataatc cgtgagctgt ctgactacact gcttcaagat taccctgtca 2160
 ccgtggcctc caacctgcag gacgaggaggc tctgggggg cctctggcgg ctggcctctgg 2220
 cacagcgctg gatggagcgg ctcaagactg tcgctgggtc caagatgcaa ggcttgcgg 2280
 agcgcgtgaa cacggagata cacttgtca ccaaatgtgc ctttcagccc ccccccagct 2340
 gtcttcgtctt cgtccagacc aacatctccc gcctcctgca ggagacctcc gagcagctgg 2400
 tggcgctgaa gcccctggatc actcgccaga acttctcccg gtgcctggag ctgcagtgtc 2460
 agcccgactc ctcaaccctg ccaccccat ggagtccccg gcccctggag gcccacagccc 2520
 cgacagcccc gtga 2534

<210> 32
 <211> 639
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 32
 Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
 1 5 10 15
 Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
 20 25 30
 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
 50 55 60
 Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn

65	70	75	80
Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser			
85	90	95	
Thr Ala Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val			
100	105	110	
Tyr Tyr Cys Val Tyr Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp			
115	120	125	
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro			
130	135	140	
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr			
145	150	155	160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr			
165	170	175	
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro			
180	185	190	
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr			
195	200	205	
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn			
210	215	220	
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser			
225	230	235	240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu			
245	250	255	
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu			
260	265	270	
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser			
275	280	285	
His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu			
290	295	300	
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr			
305	310	315	320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn			
325	330	335	
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro			
340	345	350	
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln			
355	360	365	
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val			
370	375	380	
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val			
385	390	395	400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro			
405	410	415	
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr			
420	425	430	
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val			
435	440	445	
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu			
450	455	460	
Ser Pro Gly Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly			
465	470	475	480
Gly Gly Ser Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser			
485	490	495	
Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp			
500	505	510	
Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly			
515	520	525	

Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys
 530 535 540
 Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr
 545 550 555 560
 Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys
 565 570 575
 Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser
 580 585 590
 Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser
 595 600 605
 Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro
 610 615 620
 Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro
 625 630 635

<210> 33
 <211> 1986
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 33
 atgacagtgc tggcgccagc ctggagccca acaaacctatc tcctcctgct gctgctgctg 60
 agctcgggac tcagtggac ccaggactgc tccttccaac acagccccat ctcctccgac 120
 ttcgtgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg 180
 gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctgtt cctggcacag 240
 cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc 300
 gtgaacacgg agatacactt tgtcaccaaa tgtgccttc agccccccc cagctgtctt 360
 cgcttcgtcc agaccaacat ctccccgctc ctgcaggaga cctccgagca gctggtgccg 420
 ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
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 gccccggagc ccaaatactt tgacaaaact cacacatgcc caccgtgccc agcacctgaa 600
 ctccctgggg gaccgtcagt ctccctttc cccccaaaac ccaaggacac cctcatgatc 660
 tcccgaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggta 720
 aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 780
 gagcagtaca acagcacgtc cccgggtggtc tgcgtctca ccgtcctgca ccaggactgg 840
 ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 900
 aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 960
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 ctgatctact gggcatccac taggaaatct ggtgtccctg atcgcttcac aggcagtgg 1860
 tctggacag attttactt taccatcagc agtgtacaag ctgaagaccc ggcagtttat 1920

tactgtcatc aatatttctc ctcatacacg ttccggagggg ggaccaagct ggaaataaag 1980
cggtga 1986

<210> 34
<211> 661
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 34
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Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
20 25 30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
35 40 45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
50 55 60

Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65 70 75 80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
85 90 95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
100 105 110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
115 120 125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
130 135 140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145 150 155 160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
165 170 175
Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
180 185 190
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
195 200 205
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
210 215 220
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
225 230 235 240
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
245 250 255
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
260 265 270
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
275 280 285
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
290 295 300
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
305 310 315 320
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
325 330 335
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
340 345 350

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 355 360 365
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 370 375 380
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 385 390 395 400
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Glu Val
 405 410 415
 Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val
 420 425 430
 Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Val Met
 435 440 445
 His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Asp Trp Ile Gly Tyr
 450 455 460
 Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys Gly
 465 470 475 480
 Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu
 485 490 495
 Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Tyr
 500 505 510
 Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp Gly Ala Gly Thr Thr
 515 520 525
 Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
 530 535 540
 Gly Gly Gly Ser Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala
 545 550 555 560
 Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
 565 570 575
 Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
 580 585 590
 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 595 600 605
 Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
 610 615 620
 Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
 625 630 635 640
 Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gly Thr Lys
 645 650 655
 Leu Glu Ile Lys Arg
 660

<210> 35
 <211> 426
 <212> DNA
 <213> Mus musculus

<400> 35
 gccaccatgg gattcagcag gatctttctc ttcctcctgt cagtaactac aggtgtccac 60
 tcccaggta c aactacagca gcctggggct gagctggta agcctggggc ctcagtgaag 120
 atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaaggcag 180
 acacctggc ggggcctgga atggattgga gctatttatac cagggaaatgg tgataacttcc 240
 tacaatcaga agttcaaggg caaggccaca ctgactgcag acaaattcctc cagcacagcc 300
 tacatgcagc tcagcagcct gacatctgaa gactctgcgg tctattactg tgcaagatcg 360
 acttactacg gcggtgactg gtacttcaat gtctggggcg cagggaccac ggtcaccgtc 420
 tctgca 426

<210> 36
 <211> 140
 <212> PRT
 <213> Mus musculus

<400> 36
 Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
 1 5 10 15
 Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
 20 25 30
 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
 50 55 60
 Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
 65 70 75 80
 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85 90 95
 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Ser Thr Tyr Gly Gly Asp Trp Tyr Phe Asn
 115 120 125
 Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala
 130 135 140

<210> 37
 <211> 390
 <212> DNA
 <213> Mus musculus

<400> 37
 accatggatt ttcaagtgc a gat tttcagc ttcctgctaa tcagtgc ttc agtcataatg 60
 tccagaggac aaattgttct ctcccagtct ccagcaatcc tgtctgc atc tccaggggag 120
 aaggtcacaa tgacttg cag ggccagctca agt gtaagtt acatccactg gttccagc ag 180
 aaggcaggat cctccccaa accctggatt tatgccacat ccaacctggc ttctggagtc 240
 cctgttcgct tc agtggcag tgg tctggg acctctt act ctctcacaat c agtagatg 300
 gag gctgaag atgctgccac ttattactgc c agcagtgg a ctagtaaccc acccacgttc 360
 ggtgg tggga ccaagctgg a gatcaa acga 390

<210> 38
 <211> 129
 <212> PRT
 <213> Mus musculus

<400> 38
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80

Val Arg Phe Ser Gly Ser Gly Ser Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Thr Ser Asn Pro Pro Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
115 120 125

Arg

<210> 39
<211> 2021
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 39
gccaccatgg gattcagcag gatctttctc ttccctcgt cagtaactac aggtgtccac 60
tcccaggta aactacagca gcctgggct gagctggta agcctgggc ctcagtgaag 120
atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag 180
acacctggc ggggcctgga atggatttgg a gctatttatac cagggaaatgg tgataacttcc 240
tacaatcaga agttcaaggg caaggccaca ctgactgcag acaaatacctc cagcacagcc 300
tacatgcagc tcagcagcct gacatctgaa gactctgcgg tctattactg tgcaagatcg 360
acttactacg gcggtgactg gtacttcaat gtctgggccc cagggaccac ggtcaccgtc 420
tctgcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
tctggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcttgg a actcaggcgc cctgaccaggc ggcgtgcaca cttcccccgc tgccttacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtc cttccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaaagtt 720
ggtagagggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctccgtcc 780
tggacgcattc ccggctatgc agcccccagtc cagggcagca aggccaggccc cgtctgcctc 840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggcttttc 900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc 960
aggtagctggg ctcagacact ccaagagcca tatccggag gaccctgcctc ctgacctaag 1020
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tccagtaact cccaatctt tctctgcaga gccccaaatct tgtgacaaaaa ctcacacatg 1140
cccacccgtgc ccaggtaaagc cagcccaggc ctgcctcc agctcaaggc gggacaggtg 1200
cccttagagta gcctgcattcc agggacaggc cccagccggg tgctgacacg tccacctcca 1260
tctcttcctc agcacctgaa ctccctgggg gaccgtcagt cttcccttcc ccccaaaaac 1320
ccaaaggacac cctcatgatc tcccgaccc ctgagggtcac atgcgtggtg gtggacgtga 1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
ccaaagacaaa gccgcgggag gacgactaca acagcacgtc cccgggtggc tgcgtcctca 1500
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gcaggtggca gcaggggaac gtcttctcat gtccctgtat gcatgaggct ctgcacaaacc 1980
actacacgca gaagagcctc tccctgtctc ccggtaaatg a 2021

<210> 40
<211> 470
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 40

Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
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Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
20 25 30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
50 55 60
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
65 70 75 80
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110
Tyr Tyr Cys Ala Arg Ser Thr Tyr Gly Gly Asp Trp Tyr Phe Asn
115 120 125
Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys
130 135 140
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145 150 155 160
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
165 170 175
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
180 185 190
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
195 200 205
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
210 215 220
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225 230 235 240
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
245 250 255
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
260 265 270
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
275 280 285
Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly
290 295 300
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305 310 315 320
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
325 330 335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
340 345 350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
355 360 365
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
370 375 380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385 390 395 400
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr

	405	410	415
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys			
	420	425	430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys			
	435	440	445
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu			
	450	455	460
Ser Leu Ser Pro Gly Lys			
	465	470	

<210> 41
<211> 711

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 41
accatggatt ttcaagtgc a gatttcagc ttcctgctaa tcagtgc tt c agtcataatg 60
tccagaggac aaattgttct ctccccatct ccagcaatcc t g tctgc atc tccaggggag 120
aaggtcacaa tgacttgca g gcccagctca a gtgtaagtt acatccactg gttccagcag 180
aagccaggat cctccccc a accctggatt tatgccacat ccaacctggc ttctggagtc 240
cctgttcgct tcagtggcag tgggtctggg acctttaact ctctcacaat cagtagagtg 300
gaggctgaag atgctgccac ttattactgc cagcagtgg a ctagtaaccc acccacgttc 360

ggtgggtgg a ccaagctgg a gatcaa acg a ctgtggctg caccatctgt ct tc atcttc 420
ccgc catctg atgagc agt gaaatctgg a ctgc ctctg ttgtgtgc ct gctg aataac 480
ttctatccca gagaggccaa agtac agtgg a a ggtggata acgc cctcca atc ggtaac 540
tcccaggaga gtgtcacaga gcaggac a ggc a cgc a cctac agc ctc cagc a ccc 600
ctgacgctga gca a a gca gca ctac gaga a ca caa a gtc t acgc ctgc ga a gtc a cccat 660
caggcctga gtc gcccgt ca caa a gac ttca a cagg g gaga gtt a g 711

<210> 42
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 42
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp

100	105	110
Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly	Thr Lys Leu Glu Ile Lys	
115	120	125
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe	Pro Pro Ser Asp Glu	
130	135	140
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys	Leu Leu Asn Asn Phe	
145	150	155
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp	Asn Ala Leu Gln	
165	170	175
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp	Ser Lys Asp Ser	
180	185	190
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys	Ala Asp Tyr Glu	
195	200	205
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln	Gly Leu Ser Ser	
210	215	220
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys		
225	230	235

<210> 43
<211> 2489
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 43

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gccaccatgg gattcagcag gatctttctc ttcctcctgt cagtaactac aggtgtccac 60
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atgtcctgca aggcttcgtt ctacacattt accagttaca atatgcactg gttaaagcag 180
acacctggc ggggcctgga atggatttgc gctattttc caggaaatgg tgataactcc 240
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tacatgcagc tcagcagcct gacatctgaa gactctgcgg tctattactg tgcaagatcg 360
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tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cttccagcag cttggcacc 660
cagacctaca tctgcAACGT gaatcacaag cccagcaaca ccaagggtgg caagaaaagtt 720
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cccaccgtgc ccaggtaagc cagcccaggc ctcgcctcc agctcaaggc gggacagggtg 1200
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ccctcccagc cccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtgggggtgc 1620
gaggggccaca tggacagagg ccggctcgcc ccaccctctg ccctgagagt gaccgctgtt 1680

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 gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc 1860
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 gcaggtggca gcaggggaac gtcttctcat gctccgtat gcatgaggt ctgcacaacc 1980
 actacacgca gaagagcctc tccctgtctc ccggtaaaac ccaggactgc tccttccaac 2040
 acagccccat ctccctccgac ttgcgtgtca aaatccgtga gctgtctgac tacctgcttc 2100
 aagattaccc agtcaccgtg gcctccaacc tgcaggacga ggagctctgc gggggcctct 2160
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 tggaggccac agcccccaca gccccgtga 2489

<210> 44
 <211> 626
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 44
 Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
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 Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
 20 25 30
 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
 50 55 60
 Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
 65 70 75 80
 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85 90 95
 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
 115 120 125
 Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys
 130 135 140
 Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
 145 150 155 160
 Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
 165 170 175
 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
 180 185 190
 Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
 195 200 205
 Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
 210 215 220
 Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
 225 230 235 240
 Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 245 250 255
 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp

	260	265	270												
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp
		275					280					285			
Val	Ser	His	Glu	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Asp	Gly
		290					295				300				
Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn
		305					310				315				320
Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp
		325					330				335				
Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro
		340					345				350				
Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu
		355					360				365				
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn
		370					375				380				
Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile
		385					390				395				400
Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr
		405					410				415				
Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys
		420					425				430				
Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys
		435					440				445				
Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu
		450					455				460				
Ser	Leu	Ser	Pro	Gly	Lys	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro
		465					470				475				480
Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu
		485					490				495				
Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu
		500					505				510				
Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu
		515					520				525				
Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg
		530					535				540				
Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro
		545					550				555				560
Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln
		565					570				575				
Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln
		580					585				590				
Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr
		595					600				605				
Leu	Pro	Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala	Thr	Ala	Pro	Thr
		610					615				620				
Ala	Pro														
		625													

<210> 45
<211> 2534
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 45

gccaccatgg gattcagcag gatctttctc ttcctcctgt cagtaactac aggtgtccac 60
tcccaggta aactacagca gcctgggct gagctggta agcctgggc ctcagtgaag 120
atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag 180
acacctggc ggggcctgga atggattgga gctatttatac caggaaatgg tgataactcc 240
tacaatcaga agttcaaggg caaggccaca ctgactgcag acaaattcctc cagcacagcc 300
tacatgcagc tcagcagcct gacatctgaa gactctgcgg tctattactg tgcaagatcg 360
acttactacg gcggtgactg gtacttcaat gtctggggc cagggaccac ggtcaccgtc 420
tctgcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
tctggggca cagcggccct ggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcttggg actcaggcgc cctgaccaggc ggcgtgcaca cttcccccggc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cttccagcag cttgggacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaaagtt 720
ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc 780
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cccacccaa aggccaaact ctccactccc tcagctcggc caccttctt cctccagat 1080
tccagtaact cccaatcttc tctctgcaga gcccaaattt tttttttttt tttttttttt 1140
cccaccgtgc ccaggtaagc cagcccaggc ctcgcctcc agctcaaggc gggacaggtg 1200
cccttagagta gcctgcattcc agggacaggc cccagccggg tgctgacacg tccacctca 1260
tctttcctc agcacctgaa ctctggggg gaccgtcagt cttccctttt ccccaaaaac 1320
ccaaggacac cctcatgatc tcccggaccctt ctgagggtcac atgcgtgggatgtggacgtga 1380
gccacgaaga ccctgagggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
ccaagacaaa gcccggggag gaggcgtaca acagcacgtt cccgggtggc tgcgtcctca 1500
ccgtcctgca ccaggactgg ctgaatggca aggacttacaa gtgcaaggc tccaaacaaag 1560
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gacacatcgc cgtggagtgg gagagcaatg ggcagccggaa gacaactac aagaccacgc 1860
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gcaggtggca gcaggggaaac gtcttctcat gctccgttat gcatgaggct ctgcacaacc 1980
actacacgca gaagaggctc tccctgtctc ccggtaaagg cggtggaggc tctgggtggag 2040
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ccgacttcgc tgtcaaaatc cgtgagctgt ctgactacct gttcaagat taccctgtca 2160
ccgtggcctc caacctgcag gacgaggagc tctggggggg cctctggggg ctggcctgg 2220
cacagcgctg gatggagcgg ctcaagactg tcgctgggtc caagatgcaa ggcttgcgtgg 2280
agcgcgtgaa cacggagata cactttgtca ccaaattgtgc ctttcagccc ccccccagct 2340
gtcttcgtct cgtccagacc aacatctccc gcctcctgca ggagacctcc gagecagctgg 2400
tggcgctgaa gcccggatc actcgccaga acttctcccg gtgcctggag ctgcagtgtc 2460
agcccgactc ctcaaccctg ccaccccat ggagtccccg gcccctggag gccacagccc 2520
cgacagcccc gtga 2534

<210> 46

<211> 641

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 46

Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly

1

5

10

15

Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
 20 25 30

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
 50 55 60

Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
 65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110

Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
 115 120 125

Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys
 130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
 145 150 155 160

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
 165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
 180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
 195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
 210 215 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
 225 230 235 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 245 250 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 260 265 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 275 280 285

Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly
 290 295 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 305 310 315 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 325 330 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
 340 345 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
 370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 385 390 395 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 405 410 415

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 450 455 460

Ser Leu Ser Pro Gly Lys Gly Gly Gly Ser Gly Gly Gly Ser
 465 470 475 480
 Gly Gly Gly Ser Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile
 485 490 495
 Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu
 500 505 510
 Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu
 515 520 525
 Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg
 530 535 540
 Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val
 545 550 555 560
 Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro
 565 570 575
 Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu
 580 585 590
 Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn
 595 600 605
 Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu
 610 615 620
 Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala
 625 630 635 640
 Pro

<210> 47
 <211> 1974
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 47
 atgacagtgc tggcgccagc ctggagccca acaacctatc tcctcctgct gctgctgctg 60
 agctcgggac tcagtggac ccaggactgc tccttccaac acagccccat ctcctccgac 120
 ttcgtgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg 180
 gcctccaacc tgcaaggacga ggagctctgc gggggctct ggccggctgtt cctggcacag 240
 cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc 300
 gtgaacacgg agatacacatt tgtcaccaaa tgtgccttc agccccccccc cagctgtctt 360
 cgcttcgtcc agaccaacat ctccccgtcctc ctgcaggaga cctccgagaca gctggtggcg 420
 ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
 gactcctcaa ccctgccacc cccatggagt ccccgcccccc tggaggccac agccccgaca 540
 gccccggagc ccaaattttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 600
 ctcctggggg gaccgtcagt ctcccttttcccccaaaac ccaaggacac cctcatgatc 660
 tcccgaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 720
 aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 780
 gagcagtaca acagcacgt a cccgggtggtc tgcgtcctca ccgtcctgca ccaggactgg 840
 ctgaatggca aggagtacaa gtgcaagggtc tccaacaaag ccctcccagc ccccatcgag 900
 aaaaccatct ccaaaggccaa agggcagccc cgagaaccac aggtgtacac cctggccca 960
 tcccggtatg agctgaccaa gaaccagggtc agcctgaccc gcctggtcaa aggcttctat 1020
 cccagcgaca tcgcccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1080
 acgcctcccg tgctggactc cgacggctcc ttcttcctt acagcaagct caccgtggac 1140
 aagagcaggt ggcagcaggg gaacgtcttc tcatgtccg tgatgtcatga ggctctgcac 1200
 aaccactaca cgcagaagag cctctccctg tctcccgta aacaggtaca actacagcag 1260
 cctggggctg agctggtaaa gcctggggcc tcagtgaaga tgtcctgcaa ggcttctggc 1320

tacacatcta ccagttacaa tatgcactgg gtaaaggaga cacctggcgg gggcctggaa 1380
 tggattggag ctatccatcc aggaaatggt gatacttcct acaatcgaaa gttcaagggc 1440
 aaggccacac tgactgcaga caaatcctcc agcacagcct acatgcagct cagcagcctg 1500
 acatctgaag actctgcggt ctattactgt gcaagatcga cttactacgg cggtgactgg 1560
 tacttcaatg tctggggcgc agggaccacg gtcaccgtct ctgcaggcgg tggaggctct 1620
 ggtggaggcg gttcaggagg cggtggatct caaattgttc tctccagtc tccagcaatc 1680
 ctgtctgcat ctccaggggga gaaggtcaca atgacttgcg gggccagctc aagtgtaaat 1740
 tacatccact ggttccagca gaagccagga tcctccccca aaccctggat ttatgccaca 1800
 tccaacctgg cttctggagt ccctgttcgc ttcagtgca gtgggtctgg gacctttac 1860
 tctctcacaa tcagtagagt ggaggctgaa gatgctgcca cttattactg ccagcagtgg 1920
 actagtaacc cacccacgtt cggtgggtggg accaagctgg agatcaaacg atga 1974

<210> 48
 <211> 657
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 48
 Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
 1 5 10 15
 Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
 20 25 30
 Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
 35 40 45
 Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
 50 55 60
 Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 65 70 75 80
 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
 85 90 95
 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
 100 105 110
 Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
 115 120 125
 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
 130 135 140
 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
 145 150 155 160
 Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
 165 170 175
 Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 180 185 190
 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 195 200 205
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 210 215 220
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 225 230 235 240
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 245 250 255
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 260 265 270
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 275 280 285

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 290 295 300
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 305 310 315 320
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 325 330 335
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 340 345 350
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 355 360 365
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 370 375 380
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 385 390 395 400
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gln Val
 405 410 415
 Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val
 420 425 430
 Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met
 435 440 445
 His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala
 450 455 460
 Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly
 465 470 475 480
 Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
 485 490 495
 Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
 500 505 510
 Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly
 515 520 525
 Thr Thr Val Thr Val Ser Ala Gly Gly Gly Ser Gly Gly Gly
 530 535 540
 Ser Gly Gly Gly Ser Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 545 550 555 560
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 565 570 575
 Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser
 580 585 590
 Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
 595 600 605
 Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 610 615 620
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 625 630 635 640
 Thr Ser Asn Pro Pro Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
 645 650 655

Arg

<210> 49
 <211> 426
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 49
atggattttc aggtgcagat tttcagcttc ctgctaataca gtgcctcagt cataatatcc 60
agaggagagg tttagtgggt ggagtctggc ggtggcctgg tgcagccagg gggctcactc 120
cgtttgcct gtgcagcttc tggcttcaac attaaagaca cctatataca ctgggtgcgt 180
caggccccgg gtaaggccct ggaatgggtt gcaaggattt atcctacgaa tggttatact 240
agatatgccg atagcgtcaa gggccgttac actataagcg cagacacatc caaaaacaca 300
gcctacctgc agatgaacag cctgcgtgct gaggacactg ccgtcttatta ttgttctaga 360
tggggagggg acggcttcta tgctatggac tactgggtc aaggaaccct ggtcaccgtc 420
tcctcg 426

<210> 50
<211> 142
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 50
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly
20 25 30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35 40 45
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly
50 55 60
Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr
65 70 75 80
Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
85 90 95
Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
100 105 110
Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala
115 120 125
Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
130 135 140

<210> 51
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 51
atggattttc aggtgcagat tttcagcttc ctgctaataca gtgcctcagt cataatatcc 60
agaggagaca tccagatgac ccagtcccg agctccctgt ccgcctctgt gggcgatagg 120
gttaccatca cctgccgtgc cagtcaggat gtgaataactg ctgtagcctg gtatcaacag 180
aaaccaggaa aagctccgaa actactgatt tactcggcat cttccctcta ctctggagtc 240
ccttctcgct tctctggctc cagatctggg acggatttca ctctgaccat cagcagtctg 300
cagccggaag acttcgcaac ttattactgt cagcaacatt atactactcc tcccacgttc 360
ggacagggtta ccaaggtgga gatcaaacgt 390

<210> 52
 <211> 130
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 52
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
 20 25 30
 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
 35 40 45
 Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys

50	55	60
Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val		
65	70	75
Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr		
85	90	95
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln		
100	105	110
His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile		
115	120	125
Lys Arg		
130		

<210> 53
 <211> 2021
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 53
 atggattttc aggtgcagat tttcagcttc ctgctaataca gtgcctcagt cataatatcc 60
 agaggagagg ttcaagctggt ggagtctggc ggtggcctgg tgcaaggccagg gggctcaactc 120
 cgtttgtcct gtgcagcttc tggcttcaac attaaagaca cctatataca ctgggtgcgt 180
 caggccccgg gtaaggccct ggaatgggtt gcaaggattt atcctacgaa tggttataact 240
 agatatgccg atagcgtcaa gggccgttcc actataagcg cagacacatc caaaaacaca 300
 gcctacctgc agatgaacag cctgcgtgct gaggacactg ccgtcttatta ttgttctaga 360
 tggggagggg acggcttcta tgctatggac tactgggtc aaggAACCTT ggtcaccgtc 420
 tcctcggcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
 tctggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
 gtgtcttggc actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgcctacag 600
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cttccagcag cttgggcacc 660
 cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtgga caagaaagtt 720
 ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc 780
 tggacgcattc ccggctatgc agccccagtc cagggcagca aggccaggccc cgtctgcctc 840
 ttcacccgga gcctctgccc gcccccactca tgctcaggga gagggcttcc tggcttttc 900
 ccaggctctg ggcaggcaca ggcttaggtgc ccctaaccca ggccctgcac acaaaggggc 960
 aggtgctggg ctcagacactg ccaagagcca tatccgggag gaccctgccc ctgacctaag 1020
 cccaccccaa aggccaaact ctccactccc tcagctcggaa caccttctct cctccagat 1080

tccagtaact	cccaatcttc	tctctgcaga	gcccaaatct	tgtgacaaaa	ctcacacatg	1140
cccaccgtgc	ccaggtAACG	cagccccaggc	ctcgccctcc	agctcaaggc	gggacagggtg	1200
cccttagagta	gcctgcATCC	agggacaggc	cccagccggg	tgctgacacg	tccacctcca	1260
tctcttcctc	agcacctgaa	ctcctggggg	gaccgtcagt	tttctcttcc	cccccaaaac	1320
ccaaggacac	cctcatgatc	tcccggaccc	ctgaggtcac	atgcgtggtg	gtggacgtga	1380
gccacgaaga	ccctgaggTC	aagttcaact	gttacgtgga	cggcgtggag	gtgcataatg	1440
ccaagacaaa	gccgcgggag	gagcagtaca	acagcacgta	ccgggtggtc	tgcgtcctca	1500
ccgtcctgca	ccaggactgg	ctgaatggca	aggagtacaa	gtgcaaggtc	tccaacaaag	1560
ccctcccgac	ccccatcgag	aaaacatct	ccaaagccaa	aggtgggacc	cgtgggtgc	1620
gagggccaca	tgacagaggg	ccggctcggc	ccaccctctg	ccctgagagt	gaccgctgt	1680
ccaacctctg	tcttacaggg	cagccccgag	aaccacaggt	gtacaccctg	ccccatccc	1740
gggatgagct	gaccaagaac	caggtcagcc	tgacctgct	ggtcaaaggc	ttctatccca	1800
gcgacatcgc	cgtggagtgg	gagagaatg	ggcagccgga	gaacaactac	aagaccacgc	1860
ctccccgtgct	ggactccgac	ggctccttct	ttctctacag	caagctcacc	gtggacaaga	1920
gcaggtggca	gcagggaaac	gtcttctcat	gtccgtgat	gcatgaggct	ctgcacaacc	1980
actacacqca	qaqqaqcctc	tccctgtctc	ccggtaaatg	a		2021

<210> 54
<211> 472
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 54
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser

1	5	10	15
Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly			
20	25		30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly			
35	40		45
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly			
50	55	60	
Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr			
65	70	75	80
Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr			
85	90		95
Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp			
100	105		110
Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala			
115	120		125
Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser			
130	135	140	
Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr			
145	150	155	160
Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro			
165	170		175
Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val			
180	185		190
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser			
195	200		205
Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile			
210	215	220	
Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val			
225	230	235	240

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 245 250 255
 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 260 265 270
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 275 280 285
 Val Asp Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 290 295 300
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 305 310 315 320
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 325 330 335
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 340 345 350
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 355 360 365
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 370 375 380
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 385 390 395 400
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 405 410 415
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 420 425 430
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 435 440 445
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 450 455 460
 Ser Leu Ser Leu Ser Pro Gly Lys
 465 470

<210> 55
 <211> 711
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 55
 atggatttcc aggtgcagat tttcagcttc ctgctaatca gtgcctcagt cataatatcc 60
 agaggagaca tccagatgac ccagtccccg agctccctgt cccgcctctgt gggcgatagg 120
 gttaccatca cctgccgtgc cagtcaggat gtgaatactg ctgttagcctg gtatcaacag 180
 aaaccaggaa aagctccgaa actactgatt tactcggcat ccttcctcta ctctggagtc 240
 ccttctcgct tctctggctc cagatctggg acggatttca ctctgaccat cagcagtctg 300
 cagccgaaag acttcgcaac ttattactgt cagcaacatt atactactcc tcccacgttc 360
 ggacagggtta ccaagggtga gatcaaacgt actgtggctg caccatctgt ctcatcttc 420
 ccccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480
 ttctatccca gagaggccaa agtacagtgg aaggtggata acgcctcca atcggttaac 540
 tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600
 ctgacgctga gcaaagcaga ctacgagaaa cacaagtct acgcctgcga agtcacccat 660
 cagggcctga gctcgccgt cacaagagc ttcaacaggg gagagtgtta g 711

<210> 56
 <211> 236
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 56

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5					10					15	
Val	Ile	Ile	Ser	Arg	Gly	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser
							20			25				30	
Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser
							35			40			45		
Gln	Asp	Val	Asn	Thr	Ala	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys
							50			55			60		
Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ser	Ala	Ser	Phe	Leu	Tyr	Ser	Gly	Val
	65					70				75				80	
Pro	Ser	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr
							85			90			95		
Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln
							100			105			110		
His	Tyr	Thr	Thr	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile
							115			120			125		
Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp
							130			135			140		
Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn
	145						150			155				160	
Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu
							165			170			175		
Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp
							180			185			190		
Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr
							195			200			205		
Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser
	210						215			220					
Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys				
	225					230			235						

<210> 57

<211> 2489

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 57

atggatttgc aggtgcagat tttcagcttc ctgctaatca gtgcctcagt cataatatcc 60
agaggagagg ttca gcttgggt ggagtctggc ggtggcctgg tgca gcccagg gggctca ctc 120
cgtttgcctt gtgcagcttc tggcttcaac attaaagaca cctataataca ctgggtgcgt 180
caggccccgg gtaaggccct ggaatgggtt gcaaggattt atcctacgaa tggttataact 240
agatatgcgg atagcgtcaa gggccgttcc actataagcg cagacacatc caaaaacaca 300
gcctacctgc agatgaacacag cctgcgtgct gaggacactg ccgtcttatta ttgttctaga 360
tggggagggg acggcttcta tgctatggac tactgggtc aaggaaccct ggtcaccgtc 420
tcctcggcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
tctggggca cagcggccctt gggctgcctg gtcaaggact acttccccga accggtgacg 540

gtgtcttggaa actcaggcgccctgaccgc ggcgtgcaca cttccccgc tgcctacag 600
 tcctcaggac tctactccct cagcagcggtgc ctcagcgac cttgggcacc 660
 cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtgga caagaaaagtt 720
 ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcg cgctcctgcc 780
 tggacgcattc ccggctatgc agccccagtc cagggcagca aggccaggccc cgtctgcctc 840
 ttcacccggaa gcctctgccc gcccccactca tgctcaggaa gagggtcttc tggcttttc 900
 ccaggctctg ggcaggcaca ggctaggtgc ccctaaccctt ggcctgcac acaaaggggc 960
 aggtgctggg ctcagacactt ccaagagcata tatccgggag gaccctgccc ctgacctaag 1020
 cccaccccaa aggccaaact ctccactccc tcagctcgaa caccttctt ctcacccat 1080
 tccagtaact cccaatcttc tctctgcaga gcccaaactt tgcacaaaaa ctcacacatg 1140
 cccaccgtgc ccaggtaaagc cagcccaggc ctcgcctcc agctcaaggc gggacaggtg 1200
 cccttagatgatc gcctgcattcc agggacaggc cccagccggg tgctgacacg tccacacttca 1260
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 ccaaggacac cctcatgatc tcccgaccc ctgagggtcac atgcgtggggtg gtggacgtga 1380
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 ccgtcctgca ccaggactgg ctgaatggca aggactacaa gtgcagggtc tccacaaaag 1560
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 ggcacatcgccgtggaggtgg gagagcaatg ggcagccgaa gaacaactac aagaccacgc 1860
 ctcccgtgttggactcccgac ggctccttcttccctctacag caagctcacc gtggacaaga 1920
 gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggt ctgcacaacc 1980
 actacacgcga gaagagccctc tccctgtctc ccggtaaaac ccaggactgc tccttccaac 2040
 acagccccat ctccctccgac ttgcgtgtca aaatccgtga gctgtctgac tacctgcttc 2100
 aagattaccc agtcaccgtg gcctccaacc tgcaggacga ggagctctgc gggggcctct 2160
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 tggagctgca gtgtcagccc gactcctcaa ccctgccacc cccatggagt cccggcccc 2460
 tggaggccac agccccgaca gccccgtga 2489

<210> 58
 <211> 628
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 58
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly
 20 25 30
 Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
 35 40 45
 Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly
 50 55 60
 Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr
 65 70 75 80
 Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
 85 90 95
 Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
 100 105 110

Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala
 115 120 125
 Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 130 135 140
 Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
 145 150 155 160
 Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
 165 170 175
 Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
 180 185 190
 His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
 195 200 205
 Ser Val Val Thr Val Pro Ser Ser Leu Gly Thr Gln Thr Tyr Ile
 210 215 220
 Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
 225 230 235 240
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 245 250 255
 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 260 265 270
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 275 280 285
 Val Asp Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 290 295 300
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 305 310 315 320
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 325 330 335
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 340 345 350
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 355 360 365
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 370 375 380
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 385 390 395 400

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 405 410 415
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 420 425 430
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 435 440 445
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 450 455 460
 Ser Leu Ser Leu Ser Pro Gly Lys Thr Gln Asp Cys Ser Phe Gln His
 465 470 475 480
 Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp
 485 490 495
 Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp
 500 505 510
 Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp
 515 520 525
 Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu
 530 535 540
 Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln
 545 550 555 560

Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu
 565 570 575
 Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr
 580 585 590
 Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser
 595 600 605
 Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala
 610 615 620
 Pro Thr Ala Pro
 625

<210> 59
 <211> 2534
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 59
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 agaggagagg ttcatcggtt ggagtctggc ggtggcctgg tgcagccagg gggctcaactc 120
 cgtttgcct gtgcagcttc tggcttcaac attaaagaca cctatataca ctgggtgcgt 180
 caggccccgg gtaagggcct ggaatgggtt gcaaggattt atcctacgaa tggttatact 240
 agatatgccg atagcgtcaa gggccgtttc actataagcg cagacacatc caaaaacaca 300
 gcctacctgc agatgaacag cctgcgtgct gaggacactg ccgtctatta ttgttctaga 360
 tggggagggg acggcttcta tgctatggac tactgggtc aaggaaccct ggtcaccgtc 420
 tcctcggtctt gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
 tctggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
 gtgtcttggc actcaggcgc cctgaccaggc ggcgtgcaca cttcccgcc tgccttacag 600
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cttccagcag cttgggcacc 660
 cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720
 ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc 780
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 gccacgaaga ccctgaggc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
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agcgcgtgaa cacggagata cacttgtca ccaaatgtgc ctttcagccc ccccccaagct 2340
gtttcgctt cgtccagacc aacatctccc gcctcctgca ggagacctcc gagcagctgg 2400
tggcgctgaa gcccctggatc actcgccaga acttctcccg gtgcctggag ctgcagtgtc 2460
agcccgactc ctcAACCTG ccACCCCCAT ggagtccccg gcccctggag gccacagccc 2520
cgacagcccc gtga 2534

<210> 60
<211> 643
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 60
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly
20 25 30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35 40 45
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly
50 55 60
Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr
65 70 75 80
Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
85 90 95
Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
100 105 110
Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala
115 120 125
Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
130 135 140
Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
145 150 155 160
Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
165 170 175
Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
180 185 190
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
195 200 205
Ser Val Val Thr Val Pro Ser Ser Leu Gly Thr Gln Thr Tyr Ile
210 215 220
Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
225 230 235 240
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
245 250 255
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
260 265 270
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
275 280 285
Val Asp Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
290 295 300
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
305 310 315 320

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 325 330 335
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 340 345 350
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 355 360 365
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 370 375 380
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 385 390 395 400
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 405 410 415
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 420 425 430
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 435 440 445
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 450 455 460
 Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Ser Gly Gly Gly
 465 470 475 480
 Gly Ser Gly Gly Ser Thr Gln Asp Cys Ser Phe Gln His Ser
 485 490 495
 Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr
 500 505 510
 Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu
 515 520 525
 Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met
 530 535 540
 Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu
 545 550 555 560
 Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro
 565 570 575
 Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu
 580 585 590
 Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg
 595 600 605
 Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser
 610 615 620
 Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro
 625 630 635 640
 Thr Ala Pro

<210> 61
 <211> 1998
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 61
 atgacagtgc tggcgccagc ctggagccca acaaacctatc tcctcctgct gctgctgctg 60
 agctcgccac tcagtggac ccaggactgc tccttccaac acagccccat ctcctccgac 120
 ttcgtgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg 180
 gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag 240

cgctggatgg agcggtcaaa gactgtcgct gggccaaga tgcaaggctt gctggagcgc 300
 gtgaacacgg agatacactt tgtcacaaa tgtgccttc agccccccc cagctgtctt 360
 cgcttcgtcc agaccaacat ctcccgctc ctgcaggaga cctccgagca gctggtggcg 420
 ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
 gactcctcaa ccctgccacc cccatggagt ccccggcccc tggaggccac agccccgaca 540
 gccccggagc ccaaatttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 600
 ctcctgggg gaccgtcagt cttcctctt cccccaaaac ccaaggacac cctcatgatc 660
 tcccgaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggc 720
 aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 780
 gagcagtaca acagcacgta cccgggtgtc tgctgcctca ccgtcctgca ccaggactgg 840
 ctgaatggca aggagtacaa gtcaaggc tccaacaaag ccctcccagc ccccatcgag 900
 aaaaccatct ccaaaggccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 960
 tcccgatg agctgaccaa gaaccaggc agcctgaccc gcctggtcaa aggcttctat 1020
 cccagcgaca tcgcccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1080
 acgcctcccg tgctggactc cgacggctcc ttcttcctt acagcaagct caccgtggac 1140
 aagagcaggt ggcagcaggg gaacgtcttc tcatgtccg tgatgtcatga ggctctgcac 1200
 aaccactaca cgcagaagag cctctccctg tctccggta aagaggttca gctggtggag 1260
 tctggcggtg gcctggtgca gccagggggc tcactccgtt tgcctgtgc agcttctggc 1320
 ttcaacatta aagacaccta tataactgg gtgcgtcagg ccccggtaa gggcctggaa 1380
 tgggtgcaaa ggatttatcc tacgaatggt tatacttagat atgcccatacg cgtcaaggc 1440
 cgtttacta taagcgcaga cacatccaaa aacacagcc acctgcagat gaacagcctg 1500
 cgtgctgagg acactgcccgt ctattattgt tctagatggg gaggggacgg cttctatgct 1560
 atggactact ggggtcaagg aaccctggtc accgtctcct cggctagcac caagggccca 1620
 tcggtcgccg gtggaggc tggtgaggc ggtcaggag ggggtggatc tgacatccag 1680
 atgaccctagg ccccgagctc cctgtccgccc tctgtggcg atagggttac catcacctgc 1740
 cgtgccagtc aggatgtgaa tactgctgta gcctggatc aacagaaacc agaaaaagct 1800
 ccgaaaactac tgatttactc ggcattccttc ctctactctg gagtcccttc tcgcttctt 1860
 ggctccagat ctgggacgga tttcactctg accatcagca gtctgcagcc ggaagacttc 1920
 gcaacttatt actgtcagca acattatact actcctccca cgttcggaca gggtaccaag 1980
 gtggagatca aacgttga 1998

<210> 62
 <211> 665
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 62
 Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
 1 5 10 15
 Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
 20 25 30
 Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
 35 40 45
 Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
 50 55 60
 Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 65 70 75 80
 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
 85 90 95
 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
 100 105 110
 Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
 115 120 125
 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp

130	135	140
Ile	Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu	Leu Gln Cys Gln Pro
145	150	155
Asp Ser Ser Thr	Leu Pro Pro Pro Trp Ser Pro Arg Pro	Leu Glu Ala
165	170	175
Thr Ala Pro Thr	Ala Pro Glu Pro Lys Ser Cys Asp Lys	Thr His Thr
180	185	190
Cys Pro Pro Cys Pro Ala Pro Glu	Leu Leu Gly Gly Pro Ser Val Phe	
195	200	205
Leu Phe Pro Pro Lys Pro Lys Asp Thr	Leu Met Ile Ser Arg Thr Pro	
210	215	220
Glu Val Thr Cys Val Val Val Asp Val Ser	His Glu Asp Pro Glu Val	
225	230	235
Lys Phe Asn Trp Tyr Val Asp Gly Val	Glu Val His Asn Ala Lys Thr	
245	250	255
Lys Pro Arg Glu Glu Gln Tyr Asn Ser	Thr Tyr Arg Val Val Ser Val	
260	265	270
Leu Thr Val Leu His Gln Asp Trp	Leu Asn Gly Lys Glu Tyr Lys Cys	
275	280	285
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro	Ile Glu Lys Thr Ile Ser	
290	295	300
Lys Ala Lys Gly Gln Pro Arg Glu Pro	Gln Val Tyr Thr Leu Pro Pro	
305	310	315
Ser Arg Asp Glu Leu Thr Lys Asn Gln	Val Ser Leu Thr Cys Leu Val	
325	330	335
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val	Glu Trp Glu Ser Asn Gly	
340	345	350
Gln Pro Glu Asn Asn Tyr Lys Thr	Thr Pro Pro Val Leu Asp Ser Asp	
355	360	365
Gly Ser Phe Phe Leu Tyr Ser Lys Leu	Thr Val Asp Lys Ser Arg Trp	
370	375	380
Gln Gln Gly Asn Val Phe Ser Cys Ser	Val Met His Glu Ala Leu His	
385	390	395
Asn His Tyr Thr Gln Lys Ser Leu Ser	Leu Ser Pro Gly Lys Glu Val	
405	410	415
Gln Leu Val Glu Ser Gly Gly Leu Val	Gln Pro Gly Gly Ser Leu	
420	425	430
Arg Leu Ser Cys Ala Ala Ser Gly Phe	Asn Ile Lys Asp Thr Tyr Ile	
435	440	445
His Trp Val Arg Gln Ala Pro Gly Lys	Gly Leu Glu Trp Val Ala Arg	
450	455	460
Ile Tyr Pro Thr Asn Gly Tyr Thr Arg	Tyr Ala Asp Ser Val Lys Gly	
465	470	475
Arg Phe Thr Ile Ser Ala Asp Thr Ser	Lys Asn Thr Ala Tyr Leu Gln	
485	490	495
Met Asn Ser Leu Arg Ala Glu Asp Thr	Ala Val Tyr Tyr Cys Ser Arg	
500	505	510
Trp Gly Gly Asp Gly Phe Tyr Ala Met	Asp Tyr Trp Gly Gln Gly Thr	
515	520	525
Leu Val Thr Val Ser Ser Ala Ser Thr	Lys Gly Pro Ser Val Gly Gly	
530	535	540
Gly Gly Ser Gly Gly Ser Gly Gly	Gly Ser Asp Ile Gln	
545	550	555
Met Thr Gln Ser Pro Ser Ser Leu Ser	Ala Ser Val Gly Asp Arg Val	
565	570	575
Thr Ile Thr Cys Arg Ala Ser Gln Asp	Val Asn Thr Ala Val Ala Trp	

580	585	590
Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala		
595	600	605
Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser		
610	615	620
Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe		
625	630	635
Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly		
645	650	655
Gln Gly Thr Lys Val Glu Ile Lys Arg		
660	665	

<210> 63
<211> 1098
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 63
atgacagtgc tggcgccagc ctggagccca acaacctatc tcctcctgct gctgctgctg 60
agctcgccgac tcagtggac ccaggactgc tccttccaac acagccccat ctcctccgac 120
ttcgtgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtaccgtg 180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag 240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc 300
gtgaacacgg agatacactt tgtcacaaa tgtgccttc agccccccc cagctgtctt 360
cgcttcgtcc agaccaacat ctcccgctc ctgcaggaga cctccgagaca gctggtgccg 420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
gactcctcaa ccctgcccacc cccatggagt ccccgcccc tggaggccac agccccgaca 540
gccccggcg gtggaggctc tggtgaggc ggttcaggag gcgggtggatc tgtgagagaa 600
agaggtcctc agagagtagc agctcacata actgggacca gaggaagaag caacacattg 660
tcttctccaa actccaagaa tgaaaaggct ctggggcgca aaataaaactc ctgggaatca 720
tcaaggagtg ggcattcatt cctgagcaac ttgcacttga ggaatggtga actggtcatc 780
cataaaaaag ggttttacta catctattcc caaacataact ttgcattca ggaggaaata 840
aaagaaaaaca caaagaacga caaacaaatg gtccaatata tttacaaata cacaagttat 900
cctgacccta tattgttgat gaaaagtgtc agaaatagtt gttggtctaa agatgcagaa 960
tatggactct attccatcta tcaaggggaa atatggc ttaaggaaaa tgacagaatt 1020
tttggttctg taacaaatga gcacttgata gacatggacc atgaagccag tttttttggg 1080
gccttttttag ttggctaa 1098

<210> 64
<211> 365
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 64
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu
1 5 10 15
Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
20 25 30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
35 40 45

Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
 50 55 60
 Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 65 70 75 80
 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
 85 90 95
 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
 100 105 110
 Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
 115 120 125
 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
 130 135 140
 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
 145 150 155 160
 Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
 165 170 175
 Thr Ala Pro Thr Ala Pro Gly Gly Gly Ser Gly Gly Gly Ser
 180 185 190
 Gly Gly Gly Ser Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala
 195 200 205
 His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn
 210 215 220
 Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser
 225 230 235 240
 Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly
 245 250 255
 Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr
 260 265 270
 Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys
 275 280 285
 Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile
 290 295 300
 Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu
 305 310 315 320
 Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu
 325 330 335
 Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met
 340 345 350
 Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
 355 360 365

<210> 65
 <211> 1203
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 65
 atgacagtgc tggcgccagc ctggagccca acaaacctatc tcctcctgct gctgctgctg 60
 agctcggtac tcagtggac ccaggactgc tccttccaac acagccccat ctcctccgac 120
 ttgcgtgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg 180
 gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag 240
 cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc 300
 gtgaacacgg agatacacatt tgtcacaaa tgtgccttgc agcccccccc cagctgtctt 360

cgcttcgtcc agaccaacat ctcccgctc ctgcaggaga cctccgagca gctggggcg 420
 ctgaagccct ggatcaactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
 gactcctcaa ccctgccacc cccatggagt cccccggcccc tggaggccac agccccgaca 540
 gccccgatga agcagatcga ggacaaaatt gaggaaatcc tgtccaagat ttaccacatc 600
 gagaacgaga tcgccccggat taagaaaactc attggcgaga cctctgagga aaccatttct 660
 acagttcaag aaaagcaaca aaatatattct cccctagtga gagaaagagg tcctcagaga 720
 gtagcagctc acataactgg gaccagagga agaagcaaca cattgtcttc tccaaactcc 780
 aagaatgaaa aggctctggg ccgcaaaaata aactcctggg aatcatcaag gagtgggcat 840
 tcattcctga gcaacttgca cttgaggaat ggtgaactgg tcatccatga aaaagggttt 900
 tactacatct attcccaaac atactttcgta tttcaggagg aaataaaaga aaacacaaag 960
 aacgacaaaac aaatggtcca atatatttac aaatacacaa gttatcctga cccttatattg 1020
 ttgatgaaaa gtgctagaaa tagttgttgg tctaaagatg cagaatatgg actctattcc 1080
 atctatcaag gggaatatt tgagcttaag gaaaatgaca gaattttgt ttctgtaaca 1140
 aatgagcact tgatagacat ggaccatgaa gccagtttt ttggggcctt ttagttggc 1200
 taa 1203

<210> 66

<211> 400

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 66

Met	Thr	Val	Leu	Ala	Pro	Ala	Trp	Ser	Pro	Thr	Thr	Tyr	Leu	Leu	
1														15	
Leu	Leu	Leu	Ser	Ser	Gly	Leu	Ser	Gly	Thr	Gln	Asp	Cys	Ser	Phe	
														20	
Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu
														35	
Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu
														50	
Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
														65	
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
														85	
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
														100	
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
														115	
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
														130	
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
														145	
Asp	Ser	Ser	Thr	Leu	Pro	Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala
														165	
Thr	Ala	Pro	Thr	Ala	Pro	Met	Lys	Gln	Ile	Glu	Asp	Lys	Ile	Glu	Glu
														180	
Ile	Leu	Ser	Lys	Ile	Tyr	His	Ile	Glu	Asn	Glu	Ile	Ala	Arg	Ile	Lys
														195	
Lys	Leu	Ile	Gly	Glu	Thr	Ser	Glu	Glu	Thr	Ile	Ser	Thr	Val	Gln	Glu
														210	
Lys	Gln	Gln	Asn	Ile	Ser	Pro	Leu	Val	Arg	Glu	Arg	Gly	Pro	Gln	Arg
														225	
Val	Ala	Ala	His	Ile	Thr	Gly	Thr	Arg	Gly	Arg	Ser	Asn	Thr	Leu	Ser
														245	
														250	
														255	

Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser
 260 265 270
 Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu
 275 280 285
 Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr
 290 295 300
 Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys
 305 310 315 320
 Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro
 325 330 335
 Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys
 340 345 350
 Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu
 355 360 365
 Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu
 370 375 380
 Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
 385 390 395 400

<210> 67
 <211> 1749
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 67
 atgacagtgc tggcgccagc ctggagccca acaacctatc tcctcctgtc gctgctgctg 60
 agctcgccgac tcagtgccgac ccaggactgc tccttccaac acagccccat ctcctccgac 120
 ttgcgtgtca aaatccgtga gctgtctgac tacctgtttc aagattaccc agtcaccgtg 180
 gccttccaacc tgcaggacga ggagctctgc gggggcctct ggccgtctgg cctggcacag 240
 cgctggatgg agccggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc 300
 gtgaacacgg agatacacatt tgcacccaaa tgcgtttc agccccccccc cagctgtctt 360
 cgcttcgtcc agaccaacat ctcccgccctc ctgcaggaga cctccgagca gctggtgccg 420
 ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
 gactcctcaa ccctgcccacc cccatggagt ccccgcccccc tggaggccac agccccgaca 540
 gccccggagc ccaaattttt tgacaaaact cacacatgcc caccgtgccccc agcacctgaa 600
 ctcttggggg gaccgtcagt ctccctttc cccccaaaac ccaaggacac cctcatgatc 660
 tcccgaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggc 720
 aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 780
 gagcagtaca acagcacgtt ccgggtggtc tgcgtcctca ccgtcctgca ccaggactgg 840
 ctgaatggca aggagtacaa gtcaagggtc tccaacaaag ccctcccagc ccccatcgag 900
 aaaaccatct ccaaaggccaa agggcagccc cgagaaccac aggtgtacac cctggccccc 960
 tcccgatg agctgacccaa gaaccagggtc agcctgaccc gcctggtaaa aggcttctat 1020
 cccagcgaca tcgcccgtgga gtggggagac aatggggcagc cggagaacaa ctacaagacc 1080
 acgcctcccg tgctggactc cgacggctcc ttcttccctt acagcaagct caccgtggac 1140
 aagagcagggt ggcagcagggtt gaaacgtttc tcatgtccg tgatgtatgg cgcgttcac 1200
 aaccactaca cgcagaagag cctctccctg tctccggta aagttagagaa aagaggtcct 1260
 cagagagtag cagctcacat aactgggacc agaggaagaa gcaacacatt gtcttctcca 1320
 aactccaaga atgaaaaggc tctggccgc aaaataaaact cctggaaatc atcaaggagt 1380
 gggcattcat tcctgagcaa cttgcacttg aggaatggtg aactggtcat ccatgaaaaaa 1440
 gggtttact acatctattc ccaaacatac ttgcatttc aggaggaaat aaaagaaaaac 1500
 acaaagaacg acaaacaat ggtccaatat atttacaat acacaagtta tcctgaccct 1560
 atatttgta tgaaaagtgc tagaaatagt tggtggctta aagatgcaga atatggactc 1620

tattccatct atcaaggggg aatattttag ctttaaggaaa atgacagaat ttttgtttct 1680
gtaacaaatg agcacttgat agacatggac catgaagcca gtttttttgg ggcctttta 1740
gttggctaa 1749

<210> 68
<211> 582
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 68
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
1 5 10 15
Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
20 25 30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
35 40 45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
50 55 60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65 70 75 80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
85 90 95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
100 105 110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
115 120 125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
130 135 140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145 150 155 160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
165 170 175
Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
180 185 190
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
195 200 205
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
210 215 220
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
225 230 235 240
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
245 250 255
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
260 265 270
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
275 280 285
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
290 295 300
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
305 310 315 320
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
325 330 335
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
340 345 350

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
355 360 365
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
370 375 380
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
385 390 395 400
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Val Arg
405 410 415
Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly
420 425 430
Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu
435 440 445
Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe
450 455 460
Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys
465 470 475 480
Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu
485 490 495
Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr
500 505 510
Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg
515 520 525
Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr
530 535 540
Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser
545 550 555 560
Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe
565 570 575
Gly Ala Phe Leu Val Gly
580